IN THE SPECIFICATION:

At page 11, first paragraph, please substitute the following paragraph:

Tumor cells and normal cells may be distinguished by their epigenotype as previously outlined. Knowledge of the DNA sequence of the WT1 antisense regulatory region has made it possible to develop a PCR-based assay system to allow the determination of the methylation status of samples which will require less biological material. This method involves ~~introducing~~ modifying CpG dinulceotides which are not part of a restriction enzyme recognition sequence by treatment of genomic DNA samples with sodium-metabisulphite (Merck) thereby converting all unmethylated cytosine residues to uracil (Paulin, R., *et al.,* (1998) *Nucleic Acids Research* 8, 4777-4790). Specific regions of interest in the WT1 intronic sequence can then be amplified using primers specific for both strands of DNA. The PCR bands obtained can be directly sequenced or cloned using a commercially available vector such as pGEM-T (Promega) and analysed by DNA sequencing. Any methylated cytosine residues will remain readable as 'C' in the DNA sequences, whereas unmethylated cytosines will appear as 'T'.

At page 12, second full paragraph, please substitute the following paragraph:

Therefore, methylation state of the NRE can be used as a potential early indicator of the long term ~~diseased~~ disease prognosis. Subjects who have an unmethylated NRE can be kept under closer observation for early detection of relapse. This will maximise their chances for recovery. However, the expense of such close observation post-treatment is not necessary with subjects with ~~unmethylated~~ methylated NRE, as these patients are expected to respond well to treatment once any relapse has been detected by normal routine checking.